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TECH CENTER 1600/2900

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/117,246B

DATE: 04/03/2002

TIME: 10:30:14

Input Set : A:\50026.004001.SEQLIST.TXT

Output Set: N:\CRF3\04032002\I117246B.raw

#19/  
K.T.  
4/11  
Raw  
Seq.  
Listing

4 <110> APPLICANT: Ludevid, Doloros  
 5 Torrent, Margarita  
 6 Alvarez, Inaki  
 7 Perez, Pascual  
 9 <120> TITLE OF INVENTION: Amino acid-enriched plant protein  
 10 reserves, particularly lysine-enriched maize gamma-zein, and  
 11 plants expressing such proteins  
 14 <130> FILE REFERENCE: 50062/004001  
 16 <140> CURRENT APPLICATION NUMBER: 09/117,246B  
 17 <141> CURRENT FILING DATE: 1998-12-03  
 19 <150> PRIOR APPLICATION NUMBER: PCT/FR97/00167  
 20 <151> PRIOR FILING DATE: 1997-01-28  
 22 <150> PRIOR APPLICATION NUMBER: FR96/01004  
 23 <151> PRIOR FILING DATE: 1996-01-29  
 25 <160> NUMBER OF SEQ ID NOS: 11  
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 44  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Artificial Sequence  
 34 <220> FEATURE:  
 35 <223> OTHER INFORMATION: based on Maize  
 37 <400> SEQUENCE: 1  
 38 cgatgaattc aaaccaaagc caaagccgaa gccaaaagaa ttca  
 40 <210> SEQ ID NO: 2  
 41 <211> LENGTH: 46  
 42 <212> TYPE: DNA  
 43 <213> ORGANISM: Artificial Sequence  
 45 <220> FEATURE:  
 46 <223> OTHER INFORMATION: based on Maize  
 48 <400> SEQUENCE: 2  
 49 agcttgaatt cttttggctt cggtttggc tttggttga attcat  
 51 <210> SEQ ID NO: 3  
 52 <211> LENGTH: 17  
 53 <212> TYPE: PRT  
 54 <213> ORGANISM: Maize  
 56 <400> SEQUENCE: 3  
 57 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln  
 58 1 5 10 15  
 59 Pro  
 63 <210> SEQ ID NO: 4  
 64 <211> LENGTH: 28  
 65 <212> TYPE: PRT

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66 <213> ORGANISM: Maize
68 <400> SEQUENCE: 4
69 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro
70 1 5 10 15
71 Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln Pro
72 20 25
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 20
77 <212> TYPE: PRT
78 <213> ORGANISM: Maize
80 <400> SEQUENCE: 5
81 Asp Gly Ile Asp Glu Phe Lys Pro Lys Pro Lys Pro Lys Pro Lys Glu
82 1 5 10 15
83 Phe Lys Leu Asp
84 20
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 672
89 <212> TYPE: DNA
90 <213> ORGANISM: Maize
92 <220> FEATURE:
93 <221> NAME/KEY: CDS
94 <222> LOCATION: (1)...(672)
96 <400> SEQUENCE: 6
97 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
98 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
99 1 5 10 15
101 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
102 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
103 20 25 30
105 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
106 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
107 35 40 45
109 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc 192
110 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
111 50 55 60
113 cac ctg cca ccg ccg gtc cat gtg ccg ccg ccg gtt cat ctg ccg ccg 240
114 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
115 65 70 75 80
117 cca cca tgc cac tac cct act caa ccg ccc cgg cct cag cct cat ccc 288
118 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro
119 85 90 95
121 cag cca cac cca tgc ccg tgc caa cag ccg cat cca agc ccg tgc cag 336
122 Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln
123 100 105 110
125 ctg cag gga acc tgc ggc gtt ggc agc acc ccg atc ctg ggc cag tgc 384
126 Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys
127 115 120 125
129 gtc gag ttt ctg agg cat cag tgc agc ccg acg gcg acg ccc tac tgc 432
130 Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys

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131      130      135      140
133 tcg cct cag tgc cag tcg ttg cgg cag cag tgt tgc cag cag ctc agg 480
134 Ser Pro Gln Cys Gln Ser Leu Arg Gln Gln Cys Cys Gln Gln Leu Arg
135 145      150      155      160
137 cag gtg gag ccg cag cac cgg tac cag gcg atc ttc ggc ttg gtc ctc 528
138 Gln Val Glu Pro Gln His Arg Tyr Gln Ala Ile Phe Gly Leu Val Leu
139      165      170      175
141 cag tcc atc ctg cag cag cag ccg caa agc ggc cag gtc gcg ggg ctg 576
142 Gln Ser Ile Leu Gln Gln Gln Pro Gln Ser Gly Gln Val Ala Gly Leu
143      180      185      190
145 ttg gcg gcg cag ata gcg cag caa ctg acg gcg atg tgc ggc ctg cag 624
146 Leu Ala Ala Gln Ile Ala Gln Gln Leu Thr Ala Met Cys Gly Leu Gln
147      195      200      205
149 cag ccg act cca tgc ccc tac gct gct gcc ggc ggt gtc ccc cac tga 672
150 Gln Pro Thr Pro Cys Pro Tyr Ala Ala Ala Gly Gly Val Pro His *
151 210      215      220
155 <210> SEQ ID NO: 7
156 <211> LENGTH: 223
157 <212> TYPE: PRT
158 <213> ORGANISM: Maize
160 <400> SEQUENCE: 7
161 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
162 1 5 10 15
163 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
164 20 25 30
165 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
166 35 40 45
167 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
168 50 55 60
169 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
170 65 70 75 80
171 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro
172 85 90 95
173 Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln
174 100 105 110
175 Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys
176 115 120 125
177 Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys
178 130 135 140
179 Ser Pro Gln Cys Gln Ser Leu Arg Gln Gln Cys Cys Gln Gln Leu Arg
180 145 150 155 160
181 Gln Val Glu Pro Gln His Arg Tyr Gln Ala Ile Phe Gly Leu Val Leu
182 165 170 175
183 Gln Ser Ile Leu Gln Gln Gln Pro Gln Ser Gly Gln Val Ala Gly Leu
184 180 185 190
185 Leu Ala Ala Gln Ile Ala Gln Gln Leu Thr Ala Met Cys Gly Leu Gln
186 195 200 205
187 Gln Pro Thr Pro Cys Pro Tyr Ala Ala Ala Gly Gly Val Pro His
188 210 215 220

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191 <210> SEQ ID NO: 8
192 <211> LENGTH: 693
193 <212> TYPE: DNA
194 <213> ORGANISM: maize
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (1)...(693)
200 <400> SEQUENCE: 8
201 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
202 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
203 1 5 10 15
205 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
206 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
207 20 25 30
209 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
210 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
211 35 40 45
213 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc 192
214 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
215 50 55 60
217 cac ctg cca ccg ccg gtc cat gtg ccg ccg ccg gtt cat ctg ccg ccg 240
218 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
219 65 70 75 80
221 cca cca tgc cac tac cct act caa ccg ccc cgg atc gaa ttc aaa cca 288
222 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
223 85 90 95
225 aag cca aag ccg aag cca aaa gaa ttc aaa cca aag cca aag ccg aag 336
226 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
227 100 105 110
229 cca aaa gaa ttc ctg cag ccc ctg cag gga acc tgc ggc gtt ggc agc 384
230 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
231 115 120 125
233 acc ccg atc ctg ggc cag tgc gtc gag ttt ctg agg cat cag tgc agc 432
234 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
235 130 135 140
237 ccg acg gcg acg ccc tac tgc tcg cct cag tgc cag tcg ttg cgg cag 480
238 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
239 145 150 155 160
241 cag tgt tgc cag cag ctc agg cag gtg gag ccg cag cac cgg tac cag 528
242 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
243 165 170 175
245 gcg atc ttc ggc ttg gtc ctc cag tcc atc ctg cag cag cag ccg caa 576
246 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
247 180 185 190
249 agc ggc cag gtc gcg ggg ctg ttg gcg gcg cag ata gcg cag caa ctg 624
250 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
251 195 200 205
253 acg gcg atg tgc ggc ctg cag cag ccg act cca tgc ccc tac gct gct 672
254 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala

```

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255      210      215      220      693
257 gcc ggc ggt gtc ccc cac tga
258 Ala Gly Gly Val Pro His *
259 225      230
262 <210> SEQ ID NO: 9
263 <211> LENGTH: 230
264 <212> TYPE: PRT
265 <213> ORGANISM: maize
267 <400> SEQUENCE: 9
268 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
269 1      5      10      15
270 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
271      20      25      30
272 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
273      35      40      45
274 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
275      50      55      60
276 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
277 65      70      75      80
278 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
279      85      90      95
280 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
281      100     105     110
282 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
283      115     120     125
284 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
285      130     135     140
286 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
287 145     150     155     160
288 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
289      165     170     175
290 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
291      180     185     190
292 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
293      195     200     205
294 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala
295      210     215     220
296 Ala Gly Gly Val Pro His
297 225      230
300 <210> SEQ ID NO: 10
301 <211> LENGTH: 723
302 <212> TYPE: DNA
303 <213> ORGANISM: Maize
305 <220> FEATURE:
306 <221> NAME/KEY: CDS
307 <222> LOCATION: (1)...(723)
309 <400> SEQUENCE: 10
310 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
311 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser

```

**VERIFICATION SUMMARY**

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